

FIG. 1

1 TGGGGTCATCCGGGCTGTCCGAGTCCACAGGGACAAACCCAGCCCGGACGAGGTGCAC 60
61 AGCCAAACACTGAGCCCTCCTTGTCTGTCTTCTCTGGGCTCAGACCCCTTCCACACCGTTACT 120
121 CAGCCATGGCTCCAGGTCTGTCTGGATCAGCTTGGGTCCAGCTGCTGCCCATGGTGC 180
M A P G P A R I S L G S Q L L P M V P
181 CGTGCTCCTGCTGCGGGCGCAGGCTGCGGCCACAGGGGCCCTCATGGTCTCAT 240
L L L L L R G A G C G H R G P S W S S L
241 TGGCTCGGCAGCTGCCGGTCTGACAGGGGACAGGGACTCCACAGCTACCCGGGGACG 300
P S A A A G L Q G D R D S Q Q S P G D A
301 CAGCAGCCGCTGTGGGCCAGGCCCGCAGGACATGGTGTCTATCCACATGCTCAGGCTCT 360
A A A L G P G A Q D M V A I H M L R L Y
361 ATGAGAAGTACAACCGAAGAGGTGCTCCACCGGAGGAGGCAACACCGTCCGAAGCTTCC 420
E K Y N R R G A P P G G G N T V R S F R
421 GTGCCCCGGCTGGAAATGATCGACCAAAAGCCTGTGTATTCTTCAACTTGACTTCCATGC 480
A R L E M I D Q K P V Y F F N L T S M Q
481 AAGACTCAGAAATGATCCTCACAGCCGCTTCCACTTCTACTCAGAACCTCCACGGTGGC 540
D S E M I L T A A F H F Y S E P P R W P
541 CCGGGCTGGTGAGGTATTCTGCAAGCCCCGAGCTAAGAACGCATCTCGCGCTCTCTGA 600
R A G E V F C K P R A K N A S C R L L T
601 CCCCAGGGCTGCCCTGCACGCTTGCACCTAATCTTCCGCACTTCTCCCGAAGAACCGCCA 660
P G L P A R L H L I F R S L S Q N T A T
661 CTCAGGGGCTGCTCCGGGGCCATGGCCCTGAGCCCTCCACCCAGTGGCCTGTGGCAGG 720
Q G L L R G A M A L T P P P R G L W Q A
721 CCAAGGACATCTCCTCAATCATCAAGGCTGCCCGAAGGATGGAGAGCTGCTTCTCTG 780
K D I S S I I K A A R R D G E L L S A
781 CTCAGCTGGATAGTGGGAGAGGACCCCGAGTGCCACGGCCAGTTCACCATGCCCCCT 840
Q L D T G E K D P V P R P S S H M P Y
841 ATATCCTTGTCTACGCCAATGACCTGGCCCTCTCCGAACCCCAACAGTGTAGCAGTGTGCG 900
I L V Y A N D L A I S E P N S V A V S L
901 TACAGAGATACGACCCATTTCAGCTGGAGACTTTGAGCCTGGAGCAGCCCCCAACAGCT 960
Q R Y D P F P A G D F E P G A A P N S S
961 CAGCTGATCCCCGGCTGCGCAGGGGCTCAGGTGTCAAAACCCCTGCAAGACAAATGAAC 1020
A D P R V R R A A Q V S K P L Q D N E L

FIG. 2A

GDF-10	EKSMQKARRRRQWDEPRVCSRRYLKVDF-ADIGWNEWIIISPKSFDAYYACAGACEFPMKIVRPS----
GDF-1	RPRRDAEPVLGGPGGACRARRLYVSF-REVGWHRWVIAPRGFLANYOQGCALPVALSGSGGPP
GDF-3	RKRRAAISVPKGFRCNFRHRQLFINF-QDLGWHKWVIAPKGFMANVCHGECFPMTTYLNS----
GDF-9	SFNLSYFKQFLFPQNECELDHDFRLSF-SQLKWDNWIVAPHRYNPRYCKGDCPRAVRHRYGS----
BMP-2	REKRQAKHKQKRKLKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECFPLADHLNS----
BMP-4	KRSPKHHSQARKKKNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS----
Vgr-1	SRGSGSSDYNGSELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYODGECFPLNAHMNA----
Op-1	LRMANVAENSSSDQQAACKKHELYVSF-RDLGWQDWIIAPEGYAAAYCEGECAPFLNSYMNA----
BMP-5	SRMSSVGDYNTSEQQAACKKHELYVSF-RDLGWQDWIIAPEGYAAFYODGECFPLNAHMNA----
Op-2	RLPGIFDGVHSGHRQVCRRHELYVSF-QDLGWLDWIIAPQGSAYYCEGECFPLDSCMNA----
BMP-3	EQTLKARRKQWIEPRNCARRYLKVDF-ADIGWSEWIIISPKSFDAYYCSGACQFPMPSLKPS----
MIS	GPGRARQSAGATAADGPCALRELSVDL-----RAERSVLIPEYQANNQGVCGWPQSDRNPY----
Inhibin α	ALRLLQRPPEEPAAHANCRRVALNISF-QELGWERWIVYPPSFIHYCHGCGGLHIPPNLSLPV----
Inhibin βA	RRRRRGLECDGKV--NIOCKKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL----
Inhibin βB	RIRKRGLECDGRT--NLICRQOFFIDF-RLIGWNDWIIAPTGYGYNYCEGCPAYLAGVPGSAS----
Nodal	GWGRQRRRHLPDRSQLCRRVKFQVDF-NLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHP----
TGF-β1	RRALDTNYCFSSTE-KNCCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGCPYIWSLD-----
TGF-β2	KRALDAAVCFRNVQ-DNCCLRPLYIDFRDLGWK-WIHEPKGYNANFCAGACPYLWSSD-----
TGF-β3	KRALDTNYCFRNLE-ENCCVRPLYIDFRQDLGWK-WVHEPKGYANFOSGPOPYLRSAD-----

FIG. 3A

--NHATIQSI VRA-VGIVPGIPEPCV--PDKMNSLGVFL-DENRNAVLKVYPNMSVEIQAK

ALNHAVLRALMHA--AAPGAADLPCCV--PARLSPISVLFF-DNSDNVLRQYEDMVVDECCCR

-SNYAFMQALMHM--ADPKVPKANQV--PTKLSPI SMLYQ-DSDKNVILRHYEDMVDG

-PVHTMVQNIYE--KLDPSVPRPSV--PGKYSPLSVLT'I-EPDGS IAYKEYEDMTAINICK

-TNHAIVQTLNS--VNSKIPKACV--PTELSAISMLYL-DENERVLKNIQDMVEGCGA

-TNHAIQJLVNS---VNSSI PRACU--PIELSAISMLIE-DEJBRV ENNIQEIMV ESECC-
 MUMU TUVQY VHY VUREVWPKDCCH--PTKINATSVIYE-DDNSNVTLKKVBNMVVRACGCH

--INHAIVQJLVHL--MNPEIVPECCA--F IKENATISVBI! DENSNI IZK...
 TNUHAIIVQTI VHE -- INBETTVPKBCA -- PTOI.NAISVI.YE - DPSSNVI LKKYRNMVVRACGH

INHAIVQILVHF--INFEIFKFCR--PZERRR--
-TNHAIVOTIVHI---MFPDHPKBCCA==PTKLNATSVLYF-PDSSNVILKKYRNMVVRSCGH

INHAIVQIEVHE --MKPNAVPKACOA--PTKLSATSVLYY-DSSNNVILRKARNMVVKACGCH

--NHATIOSIVRA-VGWPGIPEPCDV--PEKMSSLSILFF-DENKNNVLKVYPNMTVESQACR

-GNHVVL LKMQA--RGAALARPFCV--PTAYAGKLLISLSEER--ISAHHVPMVATECOR

-PGAPPTPAQPYS-----LLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCAACI

-SFHSTVINHYRMGRGHS PFANLKSCOV --PTKLRPMSMLYY-DDGQNIKKDIQNMIVEE

-SFHTAVNQYRMGLNPGI-VNSCOL--PIKLSIMSLYF-DDEYNIVKRDVENMIVEECSF
 EPIHVTGCIYKH VQADUHVCTCAI RIKTVPI SMI YV--DNCRVLI EHHKDMVEECCG

==INHAYIQ\$TLTKR==YQUPHRVPSICQA==FVKIRF\$SMELV--DNSKVFEEHNRKDRIVFEECEE
 TCQVSKWIIAIYNG--HNBCASAPBCQV--POAIEPIPIVYV-VGBKPKV-EOI\$NMIVRSCKCS

-IUISKVLALINQ--HNFASAFECV-IQATEPLTILYY-ICKTPKI-EQLSNMIVKSCKQS
-TOHSBVI SLYNT--INPEASABCCV--SODLEPLTILYY-ICKTPKI-EQLSNMIVKSCKQS

-TTTHSTVLGLYNT--LNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSKCS

FIG. 3B

% amino acid
identity with
GDF-10

GDF-1	38%
GDF-3	37%
GDF-9	28%
BMP-2	46%
BMP-4	45%
Vgr-1	43%
OP-1	41%
BMP-5	41%
OP-2	39%
BMP-3	83%
MIS	31%
Inhibin α	28%
Inhibin β A	36%
Inhibin β B	35%
Nodal	40%
TGF- β 1	30%
TGF- β 2	30%
TGF- β 3	29%

FIG. 4

KARRKQWDEPRVCSRRYLKVDFADIGWNEWII SPKSFDAYYCAGACEFPM
 ||||:||||||||||||||||||||||||||||||||||||||||||
 KARRRQWDEPRVCSRRYLKVDFADIGWNEWII SPKSFDAYYCAGACEFPM
 PKIVRPSNHATIQSIVRAVGII PGIPEPCCVPDKMNSLGVLFLDENRNVV
 |||||:||||||||||||||||||||||||||||||||||||||
 PKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNAV
 LKVYPNMSVDTACR
 |||||:||||
 LKVYPNMSVETACR

FIG. 5

1 2 3 4

110-
84-

47-

33-

24-

16-

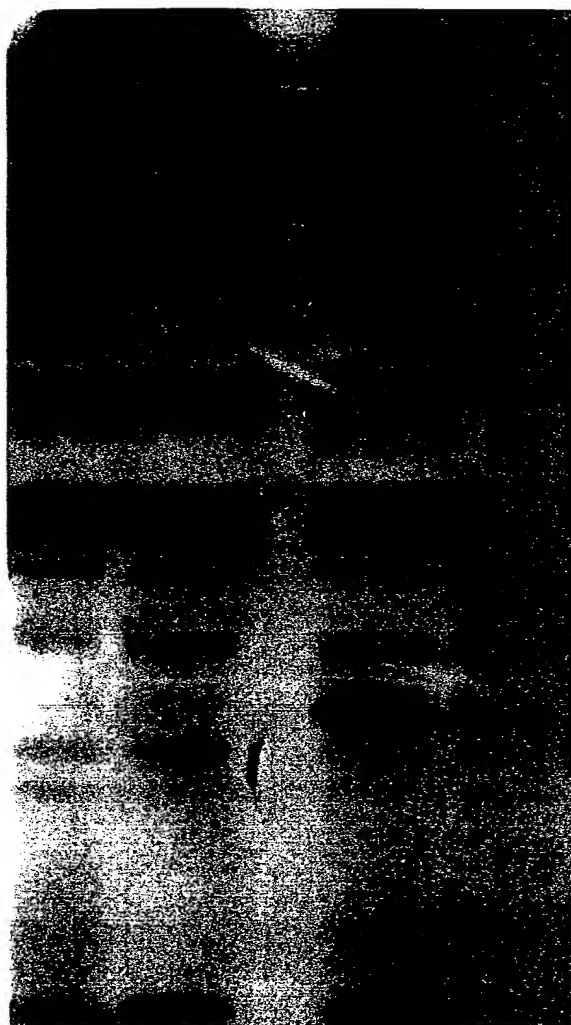


FIG. 6